

Gars Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Gars

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gars* gene. The schematic diagram is as follows:



- The *Gars* gene has 3 transcripts. According to the structure of *Gars* gene, exon2-exon3 of *Gars-201* (ENSMUST00000003572.9) transcript is recommended as the knockout region. The region contains 205bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gars* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, A dominant mutation results in sensory and motor axon degeneration in affected mice, with defects in synaptic transmission, nerve conduction and premature death. A loss of function mutation results in embryonic lethality in homozygous mice, and no discernable phenotype in heterozygous mice.
- The *Gars* gene is located on the Chr6. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Gars glycyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 353172, updated on 5-Mar-2019

Summary



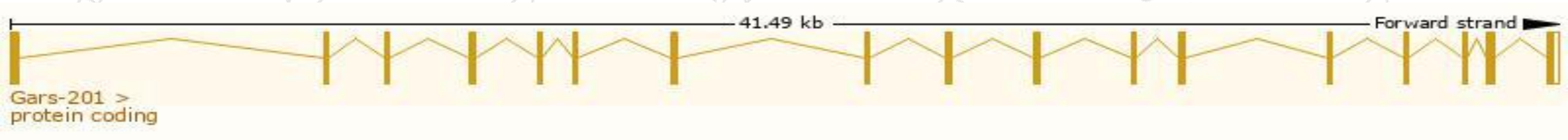
Official Symbol	Gars provided by MGI
Official Full Name	glycyl-tRNA synthetase provided by MGI
Primary source	MGI:MGI:2449057
See related	Ensembl:ENSMUSG00000029777
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	GENA202, Gena201, Nmf249, Sgrp23
Expression	Ubiquitous expression in CNS E11.5 (RPKM 46.2), CNS E18 (RPKM 40.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

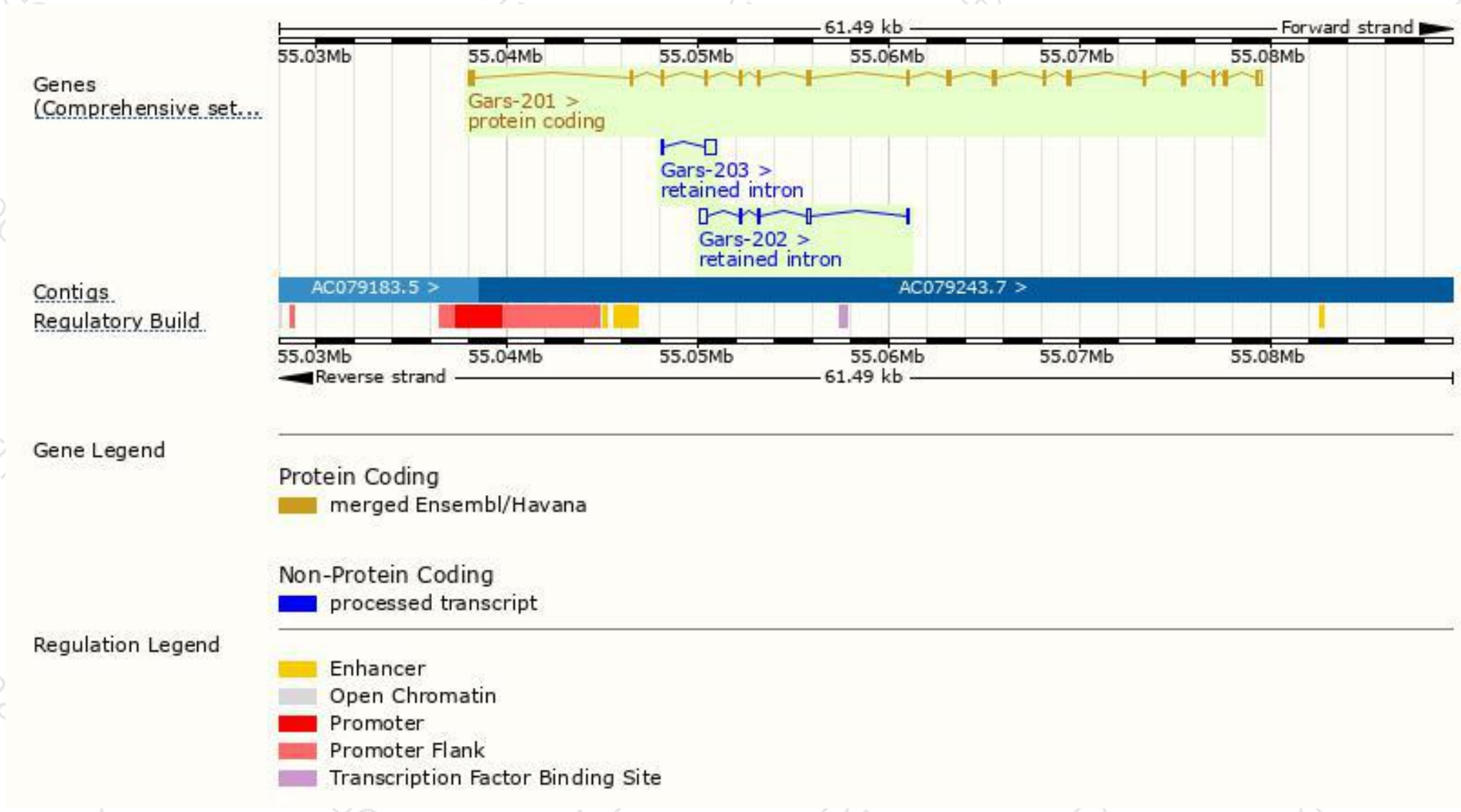
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gars-201	ENSMUST00000003572.9	2380	729aa	Protein coding	CCDS39492	Q9CZD3	TSL:1 GENCODE basic APPRIS P1
Gars-202	ENSMUST00000203334.1	834	No protein	Retained intron	-	-	TSL:2
Gars-203	ENSMUST00000205258.1	754	No protein	Retained intron	-	-	TSL:3

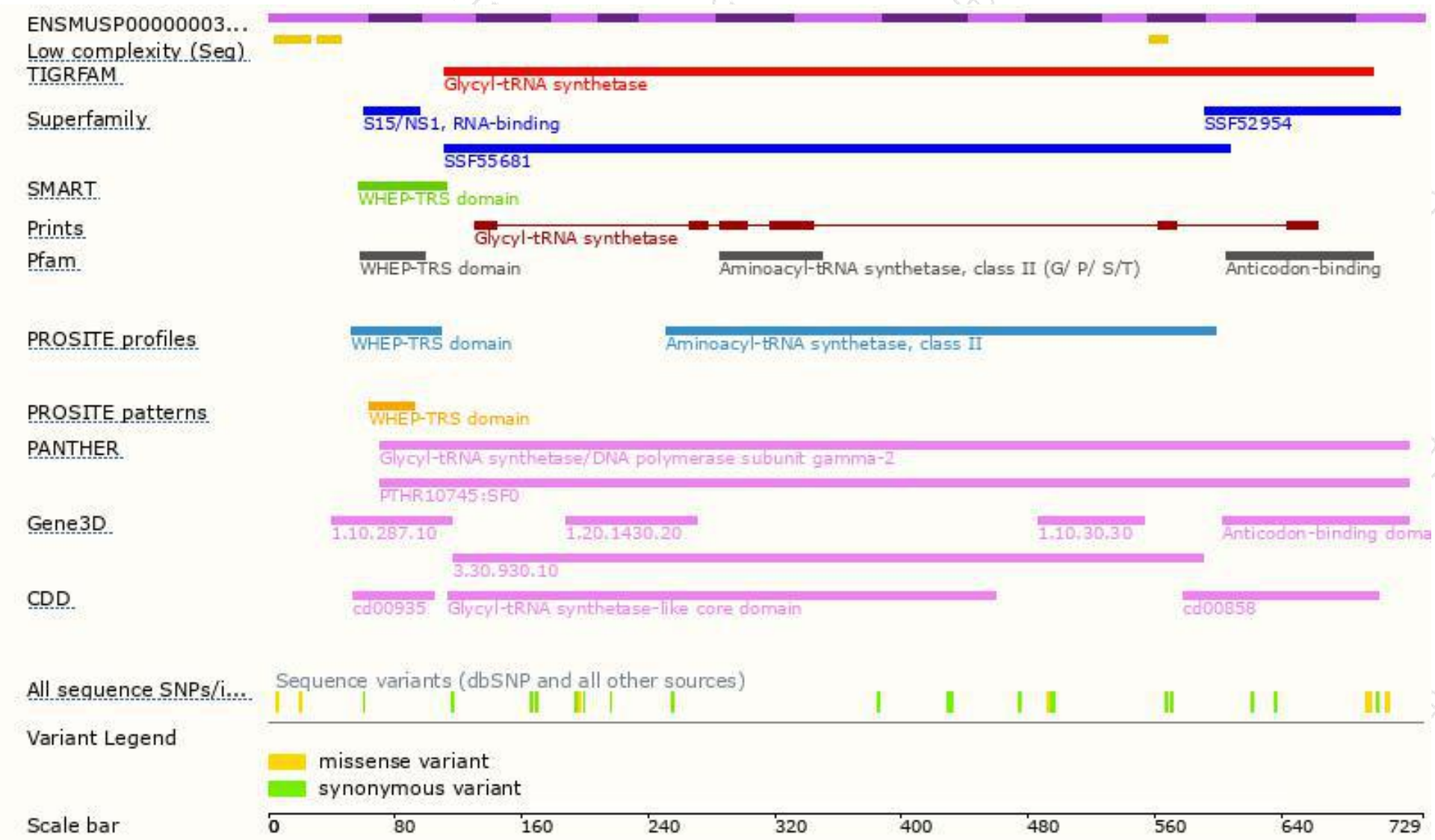
The strategy is based on the design of *Gars-201* transcript,The transcription is shown below



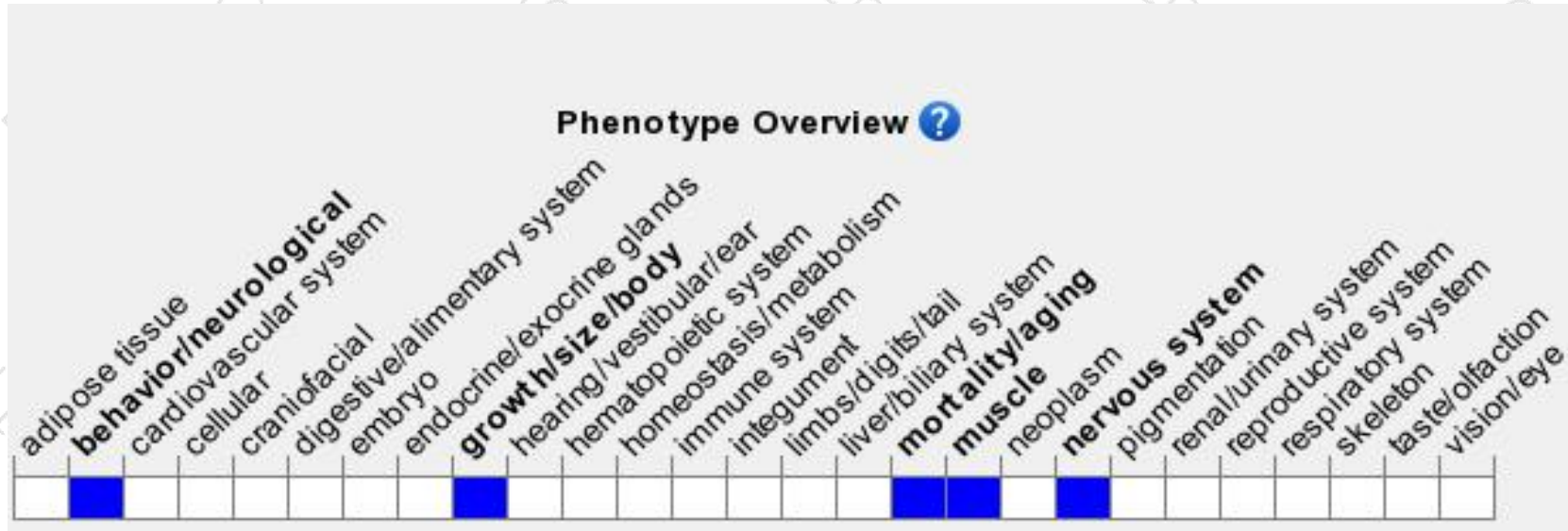
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, A dominant mutation results in sensory and motor axon degeneration in affected mice, with defects in synaptic transmission, nerve conduction and premature death. A loss of function mutation results in embryonic lethality in homozygous mice, and no discernable phenotype in heterozygous mice.

If you have any questions, you are welcome to inquire.

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